



1

SEQUENCE LISTING

COPY

<110> Blundell, Tom L
Abell, Christopher
Inoue, Tsuyoshi
von Delft, Frank

<120> Crystal Structure

<130> 620-139

<140> US 09/820,745

<141> 2001-03-30

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Conserved sequence motif

<400> 1

Leu Val Gly Asp Ser Leu Gly Met

1 5

<210> 2

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Conserved sequence motif

<400> 2

Val Lys Ile Glu Gly Gly

1 5

<210> 3

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Conserved sequence motif

<220>
<211> SITE
<222> (3)
<223> Xaa is a hydrophobic residue

<400> 3
Gly His Xaa Gly Leu Thr Pro Gln
1 5

<210> 4
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Conserved
sequence motif

<400> 4
Gly Gly Tyr Lys Val Gln Gly
1 5

<210> 5
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Conserved
sequence motif

<400> 5
Ile Gly Ile Gly Ala Gly
1 5

<210> 6
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Conserved
sequence motif

<400> 6
Asp Gly Asn Ile Leu Val
1 5

<210> 7
 <211> 264
 <212> PRT
 <213> Escherichia coli

<400> 7
 Met Lys Pro Thr Thr Ile Ser Leu Leu Gln Lys Tyr Lys Gln Asp Lys
 1 5 10 15

Lys Arg Phe Ala Thr Ile Thr Ala Tyr Asp Tyr Ser Phe Ala Lys Leu
 20 25 30

Phe Ala Asp Glu Gly Leu Asn Val Met Leu Val Gly Asp Ser Leu Gly
 35 40 45

Met Thr Val Gln Gly His Asp Ser Thr Leu Pro Val Thr Val Ala Asp
 50 55 60

Ile Ala Tyr His Thr Ala Ala Val Arg Arg Gly Ala Pro Asn Cys Leu
 65 70 75 80

Leu Leu Ala Asp Leu Pro Phe Met Ala Tyr Ala Thr Pro Glu Gln Ala
 85 90 95

Phe Glu Asn Ala Ala Thr Val Met Arg Ala Gly Ala Asn Met Val Lys
 100 105 110

Ile Glu Gly Glu Trp Leu Val Glu Thr Val Gln Met Leu Thr Glu
 115 120 125

Arg Ala Val Pro Val Cys Gly His Leu Gly Leu Thr Pro Gln Ser Val
 130 135 140

Asn Ile Phe Gly Gly Tyr Lys Val Gln Gly Arg Gly Asp Glu Ala Gly
 145 150 155 160

Asp Gln Leu Leu Ser Asp Ala Leu Ala Leu Glu Ala Ala Gly Ala Gln
 165 170 175

Leu Leu Val Leu Glu Cys Val Pro Val Glu Leu Ala Lys Arg Ile Thr
 180 185 190

Glu Ala Leu Ala Ile Pro Val Ile Gly Ile Gly Ala Gly Asn Val Thr
 195 200 205

Asp Gly Gln Ile Leu Val Met His Asp Ala Phe Gly Ile Thr Gly Gly
 210 215 220

His Ile Pro Lys Phe Ala Lys Asn Phe Leu Ala Glu Thr Gly Asp Ile
 225 230 235 240

Arg Ala Ala Val Arg Gln Tyr Met Ala Glu Val Glu Ser Gly Val Tyr
 245 250 255

Pro Gly Glu Glu His Ser Phe His
 260

<210> 8

<211> 267

<212> PRT

<213> Schizosaccharomyces pombe

<400> 8

Met	Ser	Leu	Lys	Gln	Ile	Thr	Ile	Ser	Thr	Leu	Arg	Gln	Trp	Lys	Leu
1															15

Ala	Asn	Lys	Lys	Phe	Ala	Cys	Ile	Thr	Ala	Tyr	Asp	Ala	Ser	Phe	Ser
		20											30		

Arg	Leu	Phe	Ala	Glu	Gln	Gly	Met	Pro	Val	Met	Leu	Val	Gly	Asp	Ser
													35	40	45

Leu	Gly	Met	Thr	Ala	Gln	Gly	His	Ser	Thr	Thr	Leu	Pro	Val	Ser	Val
		50											55		60

Glu	Asp	Ile	Ala	Tyr	His	Thr	Lys	Ser	Val	Arg	Arg	Gly	Ala	Pro	Asn
		65											75		80

Arg	Leu	Leu	Met	Ala	Asp	Leu	Pro	Phe	Met	Ser	Tyr	Ser	Thr	Trp	Glu
													85	90	95

Asp	Ala	Cys	Lys	Asn	Ala	Ala	Thr	Val	Met	Arg	Ala	Gly	Ala	Asn	Ile
													100	105	110

Val	Lys	Ile	Glu	Gly	Gly	Asn	Trp	Ile	Phe	Glu	Ile	Val	Gln	Arg	
		115											120		125

Leu	Thr	Glu	Arg	Ser	Val	Pro	Val	Ala	Gly	His	Leu	Gly	Leu	Thr	Pro
													130	135	140

Gln	Ser	Val	Asn	Ile	Phe	Gly	Gly	Tyr	Lys	Ile	Gln	Gly	Arg	Glu	Gln
													145	150	160

Ser	Ala	Ala	Ala	Arg	Leu	Ile	Glu	Asn	Ala	Gln	Gln	Leu	Glu	Lys	Phe
													165	170	175

Gly	Ala	Gln	Leu	Leu	Val	Leu	Glu	Cys	Ile	Pro	Glu	Ser	Leu	Ala	Glu
													180	185	190

Gln	Ile	Thr	Lys	Thr	Ile	Ser	Ile	Pro	Thr	Ile	Gly	Ile	Gly	Ala	Gly
													195	200	205

Lys	His	Thr	Asp	Gly	Gln	Ile	Leu	Val	Met	His	Asp	Ala	Leu	Gly	Ile
													210	215	220

Thr	Gly	Gly	Arg	Pro	Pro	Lys	Phe	Ala	Lys	Asn	Phe	Leu	Ser	Gly	Ala
													225	230	240

Gly	Asp	Ile	Arg	Thr	Ala	Ile	Gln	Arg	Tyr	Ile	Tyr	Glu	Val	Glu	Gln
													245	250	255

Gly	Leu	Tyr	Pro	Ala	Glu	Glu	His	Ser	Phe	Gln				
												260	265	

<210> 9
<211> 349
<212> PRT
<213> Aspergillus nidulans

<400> 9
Met Thr Phe Leu Arg Ile Ala Thr Lys Arg Ala Ile Tyr Leu His Arg
1 5 10 15
Pro Ala Asn Pro Ala Leu Pro Thr Ser Ser Ile Leu Pro Val Leu His
20 25 30
Ser Thr Asn Val Ala Thr Arg Val Pro Ser Pro Cys Ala Ile Arg His
35 40 45
Ser Ser His Ser Pro Leu Gly Ala Ala Gln Ala Asn Pro Arg Lys Lys
50 55 60
Val Thr Met Gln Thr Leu Arg Asn Leu Tyr Lys Gly Glu Pro Ile
65 70 75 80
Thr Met Leu Thr Ala His Asp Phe Pro Ser Ala His Val Ala Asp Ala
85 90 95
Ala Gly Met Asp Met Ile Leu Val Gly Asp Ser Leu Ala Met Val Ala
100 105 110
Leu Gly Met Gln Asp Thr Ser Glu Val Thr Leu Asp Asp Met Leu Val
115 120 125
His Cys Arg Ser Val Ala Arg Ala Ala Gln Ser Ala Phe Thr Val Ser
130 135 140
Asp Leu Pro Met Gly Ser Tyr Glu Val Ser Pro Glu Gln Ala Leu Gln
145 150 155 160
Ser Ala Ile Arg Ile Val Lys Glu Gly Arg Val Gln Gly Val Lys Leu
165 170 175
Glu Gly Gly Glu Glu Met Ala Pro Ala Ile Lys Arg Ile Thr Thr Ala
180 185 190
Gly Ile Pro Val Val Gly His Ile Gly Leu Thr Pro Gln Arg Gln Asn
195 200 205
Ala Leu Gly Gly Phe Arg Val Gln Gly Lys Ser Thr Thr Asp Ala Leu
210 215 220
Lys Leu Leu Lys Asp Ala Leu Ala Val Gln Glu Ala Gly Ala Phe Met
225 230 235 240
Ile Val Ile Glu Ala Val Pro Pro Glu Ile Ala Ser Ile Val Thr Gln
245 250 255
Lys Leu Ser Val Pro Thr Ile Gly Ile Gly Ala Gly Asn Gly Cys Ser
260 265 270

Gly Gln Val Leu Val Gln Ile Asp Met Thr Gly Asn Phe Pro Pro Gly
275 280 285

Arg Phe Leu Pro Lys Phe Val Lys Gln Tyr Ala Asn Val Trp Asn Glu
290 295 300

Ala Leu Gln Gly Ile Gln Gln Tyr Arg Glu Glu Val Lys Ser Arg Ala
305 310 315 320

Tyr Pro Ala Glu Gln His Thr Tyr Pro Ile Pro Lys Glu Glu Leu Val
325 330 335

Glu Phe Gln Lys Ala Val Asp Glu Leu Pro Glu Glu Lys
340 345

<210> 10

<211> 347

<212> PRT

<213> *Arabidopsis thaliana*

<400> 10

Met Ala Ser Ser Leu Thr Arg Asn Cys Ser Arg Phe Ser Lys Ala Ile
1 5 10 15

Ser Val Arg Phe Met Ser Asn Leu Pro Glu Asn Thr Val Tyr Gly Gly
20 25 30

Pro Lys Pro Gln Asn Pro Asn Gln Arg Val Thr Leu Thr His Leu Arg
 35 40 45

Gln Lys His Arg Arg Gly Glu Pro Ile Thr Val Val Thr Ala Tyr Asp
50 55 60

Tyr Pro Ser Ala Val His Leu Asp Thr Ala Gly Ile Asp Val Cys Leu
 65 70 75 80

Val Gly Asp Ser Ala Ser Met Val Val His Gly His Asp Thr Thr Leu
85 90 95

Pro Ile Ser Leu Asp Glu Met Leu Val His Cys Arg Ala Val Ala Arg
100 105 110

Gly Ala Lys Arg Pro Leu Leu Val Gly Asp Leu Pro Phe Gly Thr Tyr
115 120 125

Glu Ser Ser Ser Gln Ala Val Asp Thr Ala Val Arg Val Leu Lys
130 135 140

Glu Gly Gly Met Asp Ala Ile Lys Leu Glu Gly Gly Ser Ala Ser Arg
145 150 155 160

Ile Thr Ala Ala Lys Ala Ile Val Glu Ala Gly Ile Ala Val Ile Gly
165 170 175

His Val Gly Leu Thr Pro Gln Ala Ile Ser Val Leu Gly Gly Phe Arg
180 185 190

COPY

Pro Gln Gly Arg Asn Ile Ala Ser Ala Val Val Lys Val Glu Thr Ala
195 200 205

Met Ala Leu Gln Glu Ala Gly Cys Phe Ser Val Val Leu Glu Cys Val
210 215 220

Pro Pro Pro Val Ala Ala Ala Thr Ser Ala Leu Lys Ile Pro Thr
225 230 235 240

Ile Gly Ile Gly Ala Gly Pro Phe Cys Ser Gly Gln Val Leu Val Tyr
245 250 255

His Asp Leu Leu Gly Met Met Gln His Pro His His Ala Lys Val Thr
260 265 270

Pro Lys Phe Cys Lys Gln Tyr Ala Asn Val Gly Glu Val Ile Asn Lys
275 280 285

Ala Leu Met Glu Tyr Lys Glu Glu Val Ser Lys Lys Val Phe Pro Gly
290 295 300

Pro Ser His Ser Pro Tyr Lys Ile Thr Ala Ser Glu Leu Asp Gly Phe
305 310 315 320

Leu Thr Glu Leu Gln Lys Leu Gly Phe Asp Lys Ala Ala Ser Ala Ala
325 330 335

Ala Leu Ala Ala Glu Asn Met Glu Pro Ser Lys
340 345

<210> 11

<211> 312

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 11

Met Asn Ile Met Lys Arg Gln Leu Cys Thr Ser Ser Lys Arg Phe Phe
1 5 10 15

Ser Thr Ala Lys Asn Val Val Lys Tyr Asn Thr Ile Gln Asp Ile Arg
20 25 30

Asn Lys Tyr Phe Thr Gly Thr Pro Leu Ser Met Cys Thr Ala Tyr Asp
35 40 45

Phe Ile Thr Ala Thr Trp Val Asn Lys Ala Asn Cys Asp Leu Leu Leu
50 55 60

Val Gly Asp Ser Leu Ala Met Thr Ser Leu Gly Tyr Asp Ser Thr Ile
65 70 75 80

Thr Leu Ser Leu Asn Glu Phe Lys Tyr His Val Ala Ser Val Cys Arg
85 90 95

Ala Glu Gly Ser Ser Met Val Val Asp Met Pro Phe Gly Thr Phe
100 105 110

Glu Ser Gly Ile Ser Asp Gly Leu Lys Asn Ala Ile Asp Ile Met Lys
 115 120 125
 Leu Asp Ser Lys Val Thr Ser Val Lys Val Glu Val Gly Ser Tyr Thr
 130 135 140
 Lys Asp Lys Tyr Ala Met Lys Phe Ile Glu Glu Leu Cys Ser Arg Gly
 145 150 155 160
 Ile Pro Val Met Ala His Ile Gly Leu Thr Pro Gln Lys Val His Ser
 165 170 175
 Leu Gly Gly Tyr Lys Val Gln Gly Ser Lys Ser Leu Leu Gln Met Gln
 180 185 190
 Glu Leu Tyr Glu Thr Ala Met Gln Leu Gln Lys Ile Gly Cys Trp Ser
 195 200 205
 Ile Leu Ile Glu Cys Val Pro His Lys Met Ala Gln Phe Ile Thr Ser
 210 215 220
 Lys Leu Ser Val Pro Thr Ile Gly Ile Gly Ala Gly Asn Gly Thr Ser
 225 230 235 240
 Gly Gln Val Leu Val Ile Ser Asp Leu Leu Gly Met Gln Gly Asp Ser
 245 250 255
 Val Pro Lys Phe Val Lys Gln Ala Val Asn Met Thr Asp Ile Ala Thr
 260 265 270
 Gln Gly Leu Lys Glu Tyr Ile Ala Ser Val Glu Asp Arg Thr Phe Pro
 275 280 285
 Glu Arg Gly Thr His Thr Phe Lys Val Lys Glu Asp Leu Trp Asn Glu
 290 295 300
 Phe Leu Ser Ser Ile Asn Glu Lys
 305 310

<210> 12
 <211> 281
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Consensus

<220>
 <221> SITE
 <222> 1..4, 6..8, 10..22, 27..29, 31..39, 41, 50..52, 54..56
 <223> Xaa is uncertain

<220>
 <221> SITE
 <222> 59, 62..64, 66, 67, 69..71, 73, 76..81, 83, 88, 89
 <223> Xaa is uncertain

<220>
 <221> SITE
 <222> 91..96, 97..100, 102, 103, 105..108, 110..113, 120..133
 <223> Xaa is uncertain

<220>
 <221> SITE
 <222> 135..138, 140, 142, 145, 151..155, 163, 165..171
 <223> Xaa is uncertain

<220>
 <221> SITE
 <222> 173..175, 177, 179..181, 185, 186, 191, 194, 195
 <223> Xaa is uncertain

<220>
 <221> SITE
 <222> 198..200, 202..205, 208, 215..217, 224, 225, 227, 228
 <223> Xaa is uncertain

<220>
 <221> SITE
 <222> 230..242, 246, 248..258, 260..262, 264..266, 268..271
 <223> Xaa is uncertain

<220>
 <221> SITE
 <222> 274..277, 279..281
 <223> Xaa is uncertain

<400> 12
 Xaa Xaa Xaa Xaa Thr Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Thr Ala Tyr Asp Xaa Xaa Xaa Ala Xaa Xaa
 20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Leu Val Gly Asp Ser Leu Gly
 35 40 45

Met Xaa Xaa Xaa Gly Xaa Xaa Xaa Thr Leu Xaa Val Thr Xaa Xaa Xaa
 50 55 60

Ile Xaa Xaa His Xaa Xaa Xaa Val Xaa Arg Gly Xaa Xaa Xaa Xaa Xaa
 65 70 75 80

Xaa Leu Xaa Asp Leu Pro Phe Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa
 85 90 95

Ala Xaa Xaa Xaa Ala Xaa Xaa Val Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa
 100 105 110

Xaa Val Lys Ile Glu Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 115 120 125

Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Val Xaa Val Xaa Gly His
 130 135 140

Xaa Gly Leu Thr Pro Gln Xaa Xaa Xaa Xaa Gly Tyr Lys Val
145 150 155 160

Gln Gly Xaa Arg Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Ala
165 170 175

Xaa Ala Xaa Xaa Xaa Ala Gly Ala Xaa Xaa Leu Val Leu Glu Xaa Val
180 185 190

Pro Xaa Xaa Leu Ala Xaa Xaa Xaa Thr Xaa Xaa Xaa Xaa Ile Pro Xaa
195 200 205

Ile Gly Ile Gly Ala Gly Xaa Xaa Xaa Asp Gly Gln Ile Leu Val Xaa
210 215 220

Xaa Asp Xaa Xaa Gly Xaa
225 230 235 240

Xaa Xaa Pro Lys Phe Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
245 250 255

Xaa Xaa Ala Xaa Xaa Xaa Tyr Xaa Xaa Xaa Val Xaa Xaa Xaa Xaa Tyr
260 265 270

Pro Xaa Xaa Xaa Xaa His Xaa Xaa Xaa
275 280